

10/25#2

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/945,326

DATE: 09/20/2001

TIME: 13:49:51

Input Set : A:\Seqlist.txt

Output Set: N:\CRF3\09202001\I945326.raw

ENTERED

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4 <110> APPLICANT: Meyers, Rachel
5   Hunter, John Joseph
7 <120> TITLE OF INVENTION: 62112, A NOVEL HUMAN DEHYDROGENASE AND
8   USES THEREOF
10 <130> FILE REFERENCE: MNI-187
C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/945,326
C--> 12 <141> CURRENT FILING DATE: 2001-08-31
12 <150> PRIOR APPLICATION NUMBER: 60/229,831
13 <151> PRIOR FILING DATE: 2000-08-31
15 <160> NUMBER OF SEQ ID NOS: 3
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 2452
21 <212> TYPE: DNA
22 <213> ORGANISM: Homo sapiens
24 <220> FEATURE:
25 <221> NAME/KEY: CDS
26 <222> LOCATION: (67)...(1932)
28 <400> SEQUENCE: 1
29 cgtgtgtgtg tccctgcggc gctaagaagg ggagactgag gctgaggctg gggaacatcg 60
30 ggcagc atg agc ggc tgc ggg ctc ttc ctg cgc acc acg gct gcg gct 108
31   Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala
32       1               5               10
34 cgt gcc tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg 156
35 Arg Ala Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu
36 15               20               25               30
38 cgc acc agc ccg cct gta cga gct ttc gcc aaa gag ctt ttc cta ggc 204
39 Arg Thr Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly
40               35               40               45
42 aaa atc aag aag aaa gaa gtt ttc cca ttt cca gaa gtt agc caa gat 252
43 Lys Ile Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp
44               50               55               60
46 gaa ctt aat gaa atc aat cag ttc ttg gga ccc gtg gaa aaa ttc ttc 300
47 Glu Leu Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe
48               65               70               75
50 act gaa gag gtg gac tcc cga aaa att gac cag gaa ggg aaa atc cca 348
51 Thr Glu Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro
52 80               85               90
54 gat gaa act ttg gag aaa ttg aag agc cta ggg ctt ttt ggg ctg caa 396
55 Asp Glu Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln
56 95               100               105               110
58 gtc cca gaa gaa tat ggt ggc ctg ggc ttc tcc aac acc atg tac tca 444
59 Val Pro Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser
60               115               120               125
62 aga cta ggg gag atc atc agc atg gat ggg tcc atc act gtg acc ctg 492
63 Arg Leu Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu
64               130               135               140

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66 gca gcg cac cag gct att ggc ctc aag ggg atc atc ttg gct ggc act 540
67 Ala Ala His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr
68 145 150 155
70 gag gag cag aaa gcc aaa tac ttg cct aaa ctg gcg tcc ggg gag cac 588
71 Glu Glu Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His
72 160 165 170
74 att gca gcc ttc tgc ctc acg gag cca gcc agt ggg agc gat gca gcc 636
75 Ile Ala Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala
76 175 180 185 190
78 tca atc cgg agc aga gcc aca cta agt gaa gac aag aag cac tac atc 684
79 Ser Ile Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile
80 195 200 205
82 ctc aat ggc tcc aag gtc tgg att act aat gga gga ctg gcc aat att 732
83 Leu Asn Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile
84 210 215 220
86 ttt act gtg ttt gca aag act gag gtc gtt gat tct gat gga tca gtg 780
87 Phe Thr Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val
88 225 230 235
90 aaa gac aaa atc aca gca ttc ata gta gaa aga gac ttt ggt gga gtc 828
91 Lys Asp Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val
92 240 245 250
94 act aat ggg aaa ccc gaa gat aaa tta ggc att cgg ggc tcc aac act 876
95 Thr Asn Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr
96 255 260 265 270
98 tgt gaa gtc cat ttt gaa aac acc aag ata cct gtg gaa aac atc ctt 924
99 Cys Glu Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu
100 275 280 285
102 gga gag gtc gga gat ggg ttt aag gtg gcc atg aac atc ctc aac agc 972
103 Gly Glu Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser
104 290 295 300
106 ggc cgg ttc agc atg ggc agc gtc gtg gct ggg ctg ctc aag aga ttg 1020
107 Gly Arg Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu
108 305 310 315
110 att gaa atg act gct gag tac gcc tgc aca agg aaa cag ttt aac aag 1068
111 Ile Glu Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys
112 320 325 330
114 agg ctc agt gaa ttt gga ttg att cag gag aaa ttt gca ctg atg gct 1116
115 Arg Leu Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala
116 335 340 345 350
118 cag aag gct tac gtc atg gag agt atg acc tac ctc aca gca ggg atg 1164
119 Gln Lys Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met
120 355 360 365
122 ctg gac caa cct ggc ttt ccc gac tgc tcc atc gag gca gcc atg gtg 1212
123 Leu Asp Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val
124 370 375 380
126 aag gtg ttc agc tcc gag gcc gcc tgg cag tgt gtg agt gag gcg ctg 1260
127 Lys Val Phe Ser Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala Leu
128 385 390 395
130 cag atc ctc ggg ggc ttg ggc tac aca agg gac tat ccg tac gag cgc 1308

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131 Gln Ile Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg
132      400                      405                      410
134 ata ctg cgt gac acc cgc atc ctc ctc atc ttc gag gga acc aat gag 1356
135 Ile Leu Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu
136 415                      420                      425                      430
138 att ctc cgg atg tac atc gcc ctg acg ggt ctg cag cat gcc ggc cgc 1404
139 Ile Leu Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg
140      435                      440                      445
142 atc ctg act acc agg atc cat gag ctt aaa cag gcc aaa gtg agc aca 1452
143 Ile Leu Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr
144      450                      455                      460
146 gtc atg gat acc gtt ggc cgg agg ctt cgg gac tcc ctg ggc cga act 1500
147 Val Met Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr
148      465                      470                      475
150 gtg gac ctg ggg ctg aca ggc aac cat gga gtt gtg cac ccc agt ctt 1548
151 Val Asp Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu
152      480                      485                      490
154 gcg gac agt gcc aac aag ttt gag gag aac acc tac tgc ttc ggc cgg 1596
155 Ala Asp Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg
156 495                      500                      505                      510
158 acc gtg gag aca ctg ctg ctc cgc ttt ggc aag acc atc atg gag gag 1644
159 Thr Val Glu Thr Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu
160      515                      520                      525
162 cag ctg gta ctg aag cgg gtg gcc aac atc ctc atc aac ctg tat ggc 1692
163 Gln Leu Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly
164      530                      535                      540
166 atg acg gcc gtg ctg tcg cgg gcc agc cgc tcc atc cgc att ggg ctc 1740
167 Met Thr Ala Val Leu Ser Arg Ala Ser Arg Ser Ile Arg Ile Gly Leu
168      545                      550                      555
170 cgc aac cac gac cac gag gtt ctc ttg gcc aac acc ttc tgc gtg gaa 1788
171 Arg Asn His Asp His Glu Val Leu Leu Ala Asn Thr Phe Cys Val Glu
172      560                      565                      570
174 gct tac ttg cag aat ctc ttc agc ctc tct cag ctg gac aag tat gct 1836
175 Ala Tyr Leu Gln Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr Ala
176 575                      580                      585                      590
178 cca gaa aac cta gat gag cag att aag aaa gtg tcc cag cag atc ctt 1884
179 Pro Glu Asn Leu Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile Leu
180      595                      600                      605
182 gag aag cga gcc tat atc tgt gcc cac cct ctg gac agg aca tgc tga 1932
183 Glu Lys Arg Ala Tyr Ile Cys Ala His Pro Leu Asp Arg Thr Cys *
184      610                      615                      620
186 ggcaggggac agtgtccct gctaccgccc gccctaccc atggcccgtt gctggatgac 1992
187 tggtactctt ttttcagaag gtgttgggat tatcacaggt taagcctttt gttccccgtc 2052
188 tgcacctgaa gggttgtcgc ctggcctggg agagcctctt ccagggtttt accctgcaggc 2112
189 agtgctctct aacaggacca tcacagcttc tgaactgagc cggagagaga gaatggaatt 2172
190 gctgaccctt ggaactggcg ggtattcttg tcattgagga gacaccatag tggaaactgg 2232
191 ggcttatgct gctgcctcca ggggtgtgagg tgggtgggga cctgtgtcag gtgtggatag 2292
192 ccatttctgc tcaaccacac attctctaag aaacagcttg aaagctctgt ctgggtcatt 2352
193 catttaaaact agaagcagag gcacttaaaa catgtaccag gaaccattta acaaagaata 2412

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194 taaaatgtca caatctgtgt actgttaaaa aaaaaaaaaa
196 <210> SEQ ID NO: 2
197 <211> LENGTH: 621
198 <212> TYPE: PRT
199 <213> ORGANISM: Homo sapiens
201 <400> SEQUENCE: 2
202 Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
203 1 5 10 15
204 Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
205 20 25 30
206 Ser Pro Pro Val Arg Ala Phe Ala Lys Glu Leu Phe Leu Gly Lys Ile
207 35 40 45
208 Lys Lys Lys Glu Val Phe Pro Phe Pro Glu Val Ser Gln Asp Glu Leu
209 50 55 60
210 Asn Glu Ile Asn Gln Phe Leu Gly Pro Val Glu Lys Phe Phe Thr Glu
211 65 70 75 80
212 Glu Val Asp Ser Arg Lys Ile Asp Gln Glu Gly Lys Ile Pro Asp Glu
213 85 90 95
214 Thr Leu Glu Lys Leu Lys Ser Leu Gly Leu Phe Gly Leu Gln Val Pro
215 100 105 110
216 Glu Glu Tyr Gly Gly Leu Gly Phe Ser Asn Thr Met Tyr Ser Arg Leu
217 115 120 125
218 Gly Glu Ile Ile Ser Met Asp Gly Ser Ile Thr Val Thr Leu Ala Ala
219 130 135 140
220 His Gln Ala Ile Gly Leu Lys Gly Ile Ile Leu Ala Gly Thr Glu Glu
221 145 150 155 160
222 Gln Lys Ala Lys Tyr Leu Pro Lys Leu Ala Ser Gly Glu His Ile Ala
223 165 170 175
224 Ala Phe Cys Leu Thr Glu Pro Ala Ser Gly Ser Asp Ala Ala Ser Ile
225 180 185 190
226 Arg Ser Arg Ala Thr Leu Ser Glu Asp Lys Lys His Tyr Ile Leu Asn
227 195 200 205
228 Gly Ser Lys Val Trp Ile Thr Asn Gly Gly Leu Ala Asn Ile Phe Thr
229 210 215 220
230 Val Phe Ala Lys Thr Glu Val Val Asp Ser Asp Gly Ser Val Lys Asp
231 225 230 235 240
232 Lys Ile Thr Ala Phe Ile Val Glu Arg Asp Phe Gly Gly Val Thr Asn
233 245 250 255
234 Gly Lys Pro Glu Asp Lys Leu Gly Ile Arg Gly Ser Asn Thr Cys Glu
235 260 265 270
236 Val His Phe Glu Asn Thr Lys Ile Pro Val Glu Asn Ile Leu Gly Glu
237 275 280 285
238 Val Gly Asp Gly Phe Lys Val Ala Met Asn Ile Leu Asn Ser Gly Arg
239 290 295 300
240 Phe Ser Met Gly Ser Val Val Ala Gly Leu Leu Lys Arg Leu Ile Glu
241 305 310 315 320
242 Met Thr Ala Glu Tyr Ala Cys Thr Arg Lys Gln Phe Asn Lys Arg Leu
243 325 330 335
244 Ser Glu Phe Gly Leu Ile Gln Glu Lys Phe Ala Leu Met Ala Gln Lys

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245          340          345          350
246 Ala Tyr Val Met Glu Ser Met Thr Tyr Leu Thr Ala Gly Met Leu Asp
247          355          360          365
248 Gln Pro Gly Phe Pro Asp Cys Ser Ile Glu Ala Ala Met Val Lys Val
249          370          375          380
250 Phe Ser Ser Glu Ala Ala Trp Gln Cys Val Ser Glu Ala Leu Gln Ile
251 385          390          395          400
252 Leu Gly Gly Leu Gly Tyr Thr Arg Asp Tyr Pro Tyr Glu Arg Ile Leu
253          405          410          415
254 Arg Asp Thr Arg Ile Leu Leu Ile Phe Glu Gly Thr Asn Glu Ile Leu
255          420          425          430
256 Arg Met Tyr Ile Ala Leu Thr Gly Leu Gln His Ala Gly Arg Ile Leu
257          435          440          445
258 Thr Thr Arg Ile His Glu Leu Lys Gln Ala Lys Val Ser Thr Val Met
259          450          455          460
260 Asp Thr Val Gly Arg Arg Leu Arg Asp Ser Leu Gly Arg Thr Val Asp
261 465          470          475          480
262 Leu Gly Leu Thr Gly Asn His Gly Val Val His Pro Ser Leu Ala Asp
263          485          490          495
264 Ser Ala Asn Lys Phe Glu Glu Asn Thr Tyr Cys Phe Gly Arg Thr Val
265          500          505          510
266 Glu Thr Leu Leu Leu Arg Phe Gly Lys Thr Ile Met Glu Glu Gln Leu
267          515          520          525
268 Val Leu Lys Arg Val Ala Asn Ile Leu Ile Asn Leu Tyr Gly Met Thr
269          530          535          540
270 Ala Val Leu Ser Arg Ala Ser Arg Ser Ile Arg Ile Gly Leu Arg Asn
271 545          550          555          560
272 His Asp His Glu Val Leu Leu Ala Asn Thr Phe Cys Val Glu Ala Tyr
273          565          570          575
274 Leu Gln Asn Leu Phe Ser Leu Ser Gln Leu Asp Lys Tyr Ala Pro Glu
275          580          585          590
276 Asn Leu Asp Glu Gln Ile Lys Lys Val Ser Gln Gln Ile Leu Glu Lys
277          595          600          605
278 Arg Ala Tyr Ile Cys Ala His Pro Leu Asp Arg Thr Cys
279          610          615          620
282 <210> SEQ ID NO: 3
283 <211> LENGTH: 1863
284 <212> TYPE: DNA
285 <213> ORGANISM: Homo sapiens
287 <220> FEATURE:
288 <221> NAME/KEY: CDS
289 <222> LOCATION: (1)...(1863)
291 <400> SEQUENCE: 3
292 atg agc ggc tgc ggg ctc ttc ctg cgc acc acg gct gcg gct cgt gcc 48
293 Met Ser Gly Cys Gly Leu Phe Leu Arg Thr Thr Ala Ala Ala Arg Ala
294 1          5          10          15
296 tgc cgg ggt ctg gtg gtc tct acc gcg aac cgg cgg cta ctg cgc acc 96
297 Cys Arg Gly Leu Val Val Ser Thr Ala Asn Arg Arg Leu Leu Arg Thr
298          20          25          30

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VERIFICATION SUMMARY

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L:12 M:270 C: Current Application Number differs, Replaced Current Application No

L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date